

Figure S1 Structural characteristics of HDAC1 in different species. (A) Genomic location of human HDAC1. (B) Conserved domains of HDAC1 protein among different species. HDAC1, histone deacetylase 1.

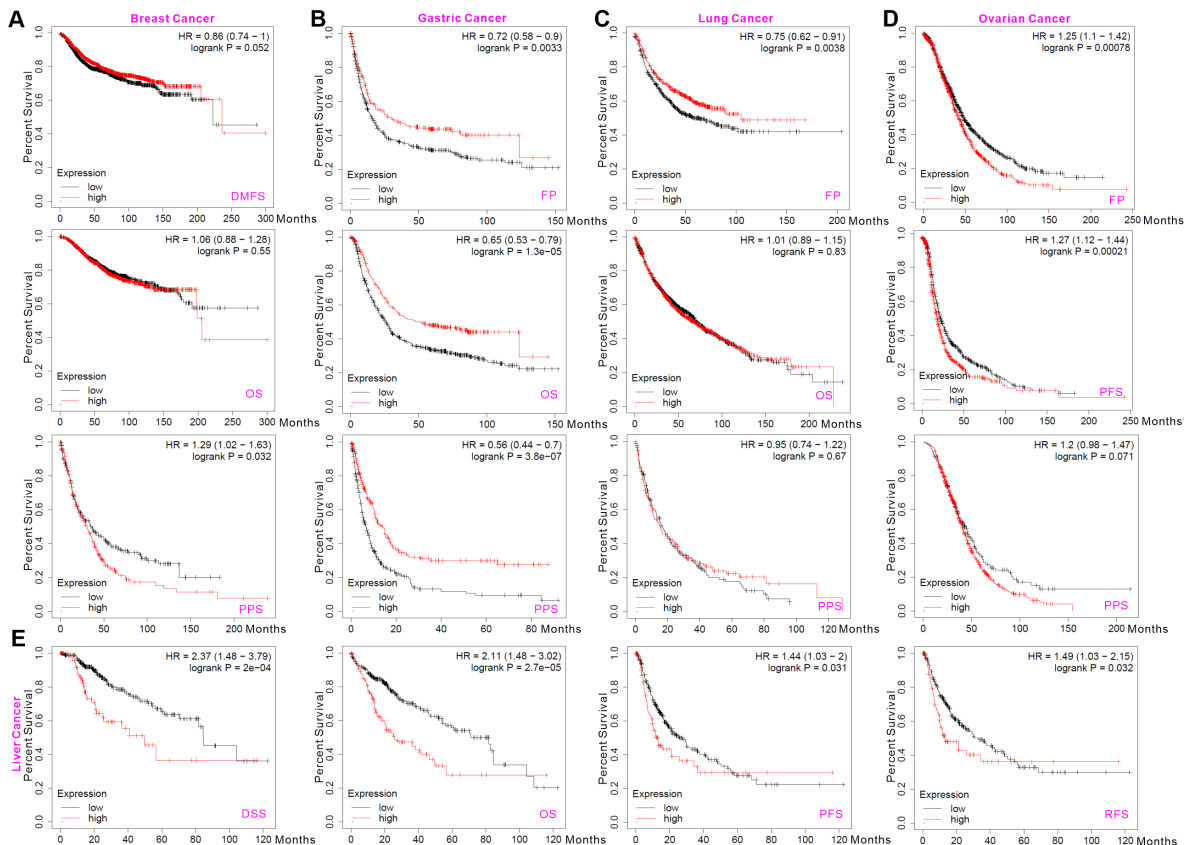


Figure S2 Correlation between HDAC1 gene expression and prognosis of cancers using the Kaplan-Meier plotter. We used the Kaplan-Meier plotter to perform a series of survival analyses, including OS, DMFS, RFS, PFS, PPS, FP, and DSS, via the expression level of the HDAC1 gene in (A) breast cancers, (B) gastric cancers, (C) lung cancers, (D) ovarian cancers, and (E) liver cancers cases. HDAC1, histone deacetylase 1; OS, overall survival; DMFS, distant metastasis-free survival; RFS, relapse-free survival; PFS, progression-free survival; PPS, post-progression survival; FP, first progression; DSS, disease-specific survival.

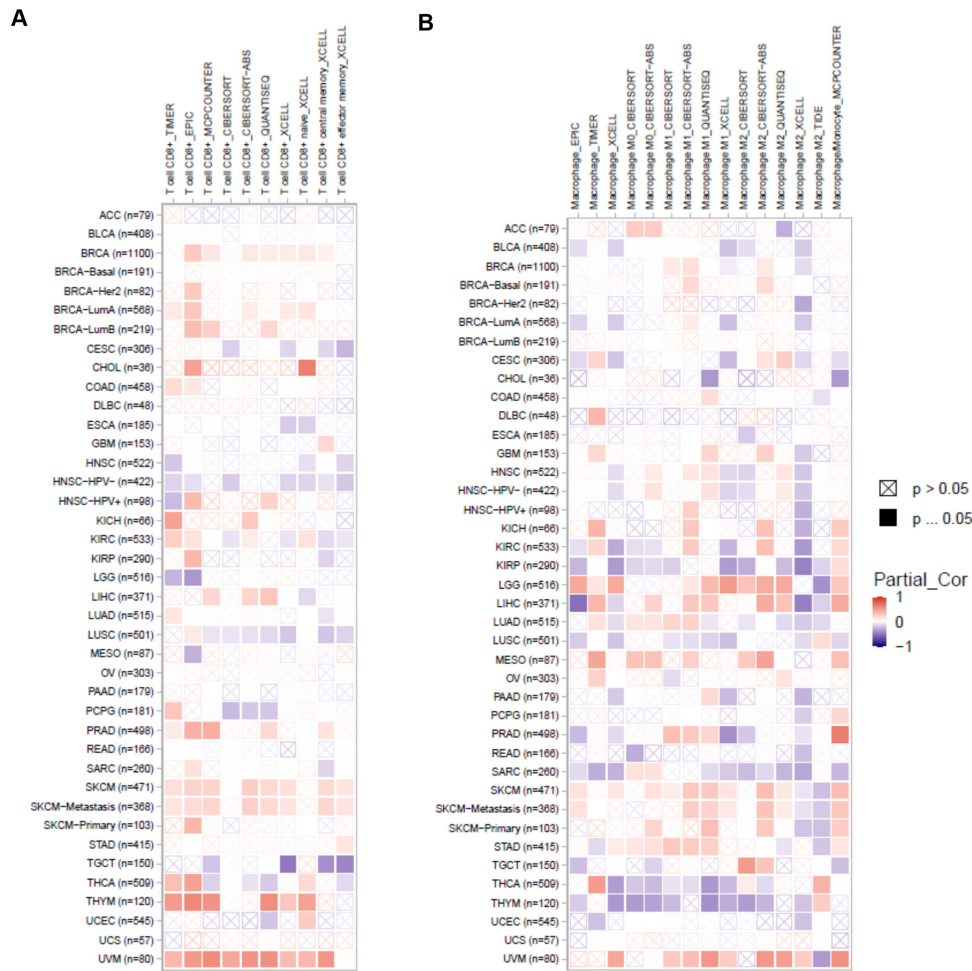


Figure S3 Correlation analysis between HDAC1 expression and immune infiltration of CD8⁺ T-cells and macrophages. (A,B) Different algorithms were used to explore the potential correlation between the expression level of HDAC1 gene and the infiltration level of CD8⁺ T-cells and macrophages across all types of cancer in TCGA datasets. HDAC1, histone deacetylase 1; TCGA, The Cancer Genome Atlas.

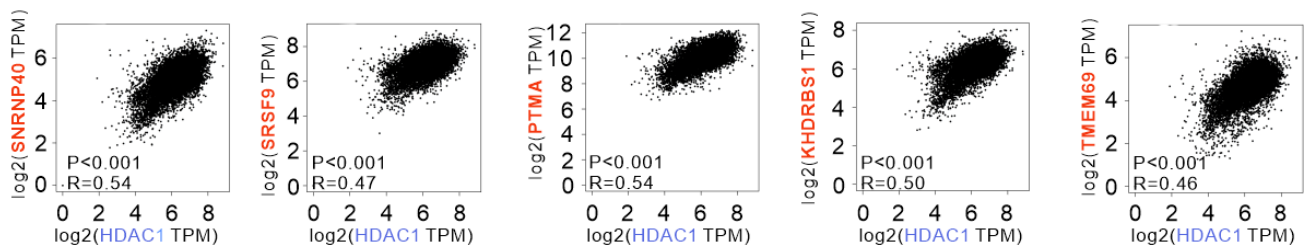


Figure S4 Enrichment analysis of HDAC1-related top 6–10 genes. The top 100 HDAC1-correlated genes in TCGA projects and analyzed the expression correlation between HDAC1 and selected targeting top 6–10 genes, including *SNRNP40*, *SRSF9*, *PTMA*, *KHDRBS1*, and *TMEM69* by the GEPIA2 approach. HDAC1, histone deacetylase 1; TCGA, The Cancer Genome Atlas; SNRNP40, small nuclear ribonucleoprotein U5 subunit 40; SRSF9, serine and arginine rich splicing factor 9; PTMA, prothymosin alpha; KHDRBS1, KH RNA binding domain containing, signal transduction associated 1; TMEM69, transmembrane protein 69; GEPIA2, Gene Expression Profiling Interactive Analysis 2.